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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=2; day=15; hr=12; min=18; sec=18; ms=279;]

=====

Reviewer Comments:

<400> 3

Met	Ala	Ser	Pro	Arg	Glu	Leu	Thr	Gln	Asn	Pro	Leu	Lys	Lys	Ile
1				5					10					15
Trp	Met	Pro	Tyr	Ser	Asn	Gly	Arg	Pro	Ala	Leu	His	Ala	Cys	Gln
				20					25					30

Please remove the blank line between the amino acids and their respective numbers above. This error appears in subsequent amino acid sequences. Also, please remove the blank lines between rows of nucleotides (this appears in subsequent sequences).

(end of Sequence 86)

ttttatttta tttatttttt gatggagtct tgcactccag cctggtgaca gact 1914

PF-1506 PCT

1/94

WASH_1695548.1

Please remove the above three lines of text, which appear at the end of the submitted file.

Application No: 10554917 Version No: 1.0

Input Set:**Output Set:**

Started: 2008-02-14 12:58:35.910
Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (3)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (7)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (13)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (15)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (16)

Input Set:

Output Set:

Started: 2008-02-14 12:58:35.910
Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (24)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (28)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (29)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (31)
E 355	Empty lines found between the amino acid numbering and the proteins
E 321	No. of Bases conflict, this line has no nucleotides SEQID (31) POS (915)
E 330	Invalid protein , found in SEQID(86) POS (1)Invalid Protein:PCT

Input Set:

Output Set:

Started: 2008-02-14 12:58:35.910
Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
W 112	Upper case found in data; Found at position(1914) SeqId(86)
W 112	Upper case found in data; Found at position(1915) SeqId(86)
W 112	Upper case found in data; Found at position(1916) SeqId(86)
W 112	Upper case found in data; Found at position(1917) SeqId(86)
E 259	Found undefined lettercode; POS (1919) SEQID(86)
E 259	Found undefined lettercode; POS (1920) SEQID(86)
E 259	Found undefined lettercode; POS (1921) SEQID(86)
E 259	Found undefined lettercode; POS (1922) SEQID(86)
E 259	Found undefined lettercode; POS (1923) SEQID(86)
E 259	Found undefined lettercode; POS (1924) SEQID(86)
E 259	Found undefined lettercode; POS (1925) SEQID(86)
E 259	Found undefined lettercode; POS (1926) SEQID(86)
E 259	Found undefined lettercode; POS (1927) SEQID(86)
E 254	The total number of bases conflicts with running total, Input: 1, Calculated : 1927 SEQID(86)
E 253	The number of bases differs from <211> Input: 1914 Calculated:1927 SEQID (86)

<110> INCYTE CORPORATION; ELLIOTT, Vicki S.;
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CHAWLA, Narinder K.; BAUGHN, Mariah R.;
LEE, Soo Yeun; TRAN, Uyen K.;
YUE, Henry; NGUYEN, Dannel B.;
THORNTON, Michael B.; GURURAJAN, Rajagopal;
GANDHI, Ameena R.; LU, Yan;
YAO, Monique G.; LI, Joana X.;
LUO, Wen; LEE, Ernestine A.;
FORSYTHE, Ian J.; ISON, Craig H.;
WILSON, Amy D.; JIN, Pei

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<130> PF-1506 PCT

<140> 10554917

<141> 2008-02-14

<150> US 60/467,491

<151> 2003-04-30

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<151> 2003-05-09

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<151> 2003-08-12

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<151> 2003-12-10

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<211> 83

<212> PRT

<213> Homo sapiens

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Asn	Ile	Asp	Val	Cys	Glu	Asn	Cys	His	Tyr	Pro	Ile	Val	Pro	Leu
				20					25					30

Asp	Gly	Lys	Gly	Thr	Leu	Leu	Ile	Arg	Asn	Gly	Ser	Glu	Thr	Thr
				35					40					45
Trp	Leu	Ser	Leu	Cys	Thr	Ala	Met	Ser	Pro	Leu	Thr	Thr	Glu	Ile
				50					55					60
Trp	Ala	Leu	Arg	Arg	Gly	Asn	Ser	Ser	Ala	Ser	Trp	Ser	Arg	Ala
				65					70					75
Ala	Ser	Gly	Gly	Arg	Arg	Ser	Pro							
				80										

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<211> 292

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7520272CD1

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Met	Ala	Asp	Gln	Ala	Pro	Phe	Asp	Thr	Asp	Val	Asn	Thr	Leu	Thr
1				5					10					15
Arg	Phe	Val	Met	Glu	Gly	Arg	Lys	Ala	Arg	Gly	Thr	Gly	Glu	
				20					25					30
Leu	Thr	Gln	Leu	Leu	Asn	Ser	Leu	Cys	Thr	Ala	Val	Lys	Ala	Ile
				35					40					45
Ser	Ser	Ala	Val	Arg	Lys	Ala	Gly	Ile	Ala	His	Leu	Tyr	Gly	Ile
				50					55					60
Ala	Gly	Ser	Thr	Asn	Val	Thr	Gly	Asp	Gln	Val	Lys	Lys	Leu	Asp
				65					70					75
Val	Leu	Ser	Asn	Asp	Leu	Val	Met	Asn	Met	Leu	Lys	Ser	Ser	Phe
				80					85					90
Ala	Thr	Cys	Val	Leu	Val	Ser	Glu	Glu	Asp	Lys	His	Ala	Ile	Ile
				95					100					105
Val	Glu	Pro	Glu	Lys	Arg	Gly	Lys	Tyr	Val	Val	Cys	Phe	Asp	Pro
				110					115					120
Leu	Asp	Gly	Ser	Ser	Asn	Ile	Asp	Cys	Leu	Val	Ser	Val	Gly	Thr
				125					130					135
Ile	Phe	Gly	Ile	Tyr	Arg	Lys	Lys	Ser	Thr	Asp	Glu	Pro	Ser	Glu
				140					145					150
Lys	Asp	Ala	Leu	Gln	Pro	Gly	Arg	Asn	Leu	Val	Ala	Ala	Gly	Tyr
				155					160					165
Ala	Leu	Tyr	Gly	Ser	Ala	Thr	Met	Leu	Val	Leu	Ala	Met	Asp	Cys
				170					175					180
Gly	Val	Asn	Cys	Phe	Met	Leu	Asp	Pro	Asp	Asn	Ser	Ala	Pro	Tyr
				185					190					195
Gly	Ala	Arg	Tyr	Val	Gly	Ser	Met	Val	Ala	Asp	Val	His	Arg	Thr
				200					205					210
Leu	Val	Tyr	Gly	Gly	Ile	Phe	Leu	Tyr	Pro	Ala	Asn	Lys	Lys	Ser
				215					220					225
Pro	Asn	Gly	Lys	Leu	Arg	Leu	Leu	Tyr	Glu	Cys	Asn	Pro	Met	Ala
				230					235					240
Tyr	Val	Met	Glu	Lys	Ala	Gly	Gly	Met	Ala	Thr	Thr	Gly	Lys	Glu
				245					250					255
Ala	Val	Leu	Asp	Val	Ile	Pro	Thr	Asp	Ile	His	Gln	Arg	Ala	Pro
				260					265					270
Val	Ile	Leu	Gly	Ser	Pro	Asp	Asp	Val	Leu	Glu	Phe	Leu	Lys	Val
				275					280					285

Tyr Glu Lys His Ser Ala Gln
290

<210> 3

<211> 434

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7521279CD1

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Trp	Met	Pro	Tyr	Ser	Asn	Gly	Arg	Pro	Ala	Leu	His	Ala	Cys	Gln
				20				25						30
Arg	Gly	Val	Cys	Met	Thr	Asn	Cys	Pro	Thr	Leu	Ile	Val	Met	Val
				35				40						45
Gly	Leu	Pro	Ala	Arg	Gly	Lys	Thr	Tyr	Ile	Ser	Lys	Lys	Leu	Thr
				50				55						60
Arg	Tyr	Leu	Asn	Trp	Ile	Gly	Val	Pro	Thr	Arg	Glu	Phe	Asn	Val
				65				70						75
Gly	Gln	Tyr	Arg	Arg	Asp	Val	Val	Lys	Thr	Tyr	Lys	Ser	Phe	Glu
				80				85						90
Phe	Phe	Leu	Pro	Asp	Asn	Glu	Glu	Gly	Leu	Lys	Ile	Arg	Lys	Gln
				95				100						105
Cys	Ala	Leu	Ala	Ala	Leu	Arg	Asp	Val	Arg	Arg	Phe	Leu	Ser	Glu
				110				115						120
Glu	Gly	Gly	His	Val	Ala	Val	Phe	Asp	Ala	Thr	Asn	Thr	Thr	Arg
				125				130						135
Glu	Arg	Arg	Ala	Thr	Ile	Phe	Asn	Phe	Gly	Glu	Gln	Asn	Gly	Tyr
				140				145						150
Lys	Thr	Phe	Phe	Val	Glu	Ser	Ile	Cys	Val	Asp	Pro	Glu	Val	Ile
				155				160						165
Ala	Ala	Asn	Ile	Val	Gln	Val	Lys	Leu	Gly	Ser	Pro	Asp	Tyr	Val
				170				175						180
Asn	Arg	Asp	Ser	Asp	Glu	Ala	Thr	Glu	Asp	Phe	Met	Arg	Arg	Ile
				185				190						195
Glu	Cys	Tyr	Glu	Asn	Ser	Tyr	Glu	Ser	Leu	Asp	Glu	Asp	Leu	Asp
				200				205						210
Arg	Asp	Leu	Ser	Tyr	Ile	Lys	Ile	Met	Asp	Val	Gly	Gln	Ser	Tyr
				215				220						225
Val	Val	Asn	Arg	Val	Ala	Asp	His	Ile	Gln	Ser	Arg	Ile	Val	Tyr
				230				235						240
Tyr	Leu	Met	Asn	Ile	His	Val	Thr	Pro	Arg	Ser	Ile	Tyr	Leu	Cys
				245				250						255
Arg	His	Gly	Glu	Ser	Glu	Leu	Asn	Leu	Lys	Gly	Arg	Ile	Gly	Gly
				260				265						270
Asp	Pro	Gly	Leu	Ser	Pro	Arg	Gly	Arg	Glu	Phe	Ala	Lys	Ser	Leu
				275				280						285
Ala	Gln	Phe	Ile	Ser	Asp	Gln	Asn	Ile	Lys	Asp	Leu	Lys	Val	Trp
				290				295						300
Thr	Ser	Gln	Met	Lys	Arg	Thr	Ile	Gln	Thr	Ala	Glu	Ala	Leu	Gly
				305				310						315
Val	Pro	Tyr	Glu	Gln	Trp	Lys	Val	Leu	Asn	Glu	Ile	Asp	Ala	Ser

	320		325		330
Tyr Glu Asp Leu Val Gln Arg Leu Glu Pro Val Ile Met Glu Leu					
	335		340		345
Glu Arg Gln Glu Asn Val Leu Val Ile Cys His Gln Ala Val Met					
	350		355		360
Arg Cys Leu Leu Ala Tyr Phe Leu Asp Lys Ala Ala Glu Gln Leu					
	365		370		375
Pro Tyr Leu Lys Cys Pro Leu His Thr Val Leu Lys Leu Thr Pro					
	380		385		390
Val Ala Tyr Gly Cys Lys Val Glu Ser Ile Phe Leu Asn Val Ala					
	395		400		405
Ala Val Asn Thr His Arg Asp Arg Pro Gln Asn Val Asp Ile Ser					
	410		415		420
Arg Pro Pro Glu Glu Ala Leu Val Thr Val Pro Ala His Gln					
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<211> 240

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

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	20	25	30
Arg Val Leu Ser Gly Asp Leu Gly Gln Leu Pro Thr Gly Ile Arg			
	35	40	45
Asp Phe Val Glu His Ser Ala Arg Leu Cys Gln Pro Glu Gly Ile			
	50	55	60
His Ile Cys Asp Gly Thr Glu Ala Glu Asn Thr Ala Thr Leu Thr			
	65	70	75
Leu Leu Glu Gln Gln Gly Leu Ile Arg Lys Leu Pro Lys Tyr Asn			
	80	85	90
Asn Cys Trp Leu Ala Arg Thr Asp Pro Lys Asp Val Ala Arg Val			
	95	100	105
Glu Ser Lys Thr Val Ile Val Thr Pro Ser Gln Arg Asp Thr Val			
	110	115	120
Pro Leu Pro Pro Gly Gly Ala Arg Gly Gln Leu Gly Asn Trp Met			
	125	130	135
Ser Pro Ala Asp Phe Gln Arg Ala Val Asp Glu Arg Phe Pro Gly			
	140	145	150
Cys Met Gln Gly Arg Thr Met Tyr Val Leu Pro Phe Ser Met Gly			
	155	160	165
Pro Val Gly Ser Pro Leu Ser Arg Ile Gly Val Gln Leu Thr Asp			
	170	175	180
Ser Ala Tyr Val Val Ala Ser Met Arg Ile Met Thr Arg Leu Gly			
	185	190	195
Thr Pro Val Leu Gln Ala Leu Gly Asp Gly Asp Phe Val Lys Cys			
	200	205	210
Leu His Ser Val Gly Gln Pro Leu Thr Gly Gln Asp Pro Gly His			
	215	220	225
His Gln Pro Cys Arg Glu Glu Ala Leu Cys Gly Ser Arg Leu Pro			

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Thr Asn Ser Pro Thr Met Val Ile Met Val Gly Leu Pro Ala Arg
             20             25             30
Gly Lys Thr Tyr Ile Ser Thr Lys Leu Thr Arg Tyr Leu Asn Trp
             35             40             45
Ile Gly Thr Pro Thr Lys Val Phe Asn Leu Gly Gln Tyr Arg Arg
             50             55             60
Glu Ala Val Ser Tyr Lys Asn Tyr Glu Phe Phe Leu Pro Asp Asn
             65             70             75
Met Glu Ala Leu Gln Ile Arg Lys Gln Cys Ala Leu Ala Ala Leu
             80             85             90
Lys Asp Val His Asn Tyr Leu Ser His Glu Glu Gly His Val Ala
             95            100            105
Val Phe Asp Ala Thr Asn Thr Thr Arg Glu Arg Arg Ser Leu Ile
            110            115            120
Leu Gln Phe Ala Lys Glu His Gly Tyr Lys Val Phe Phe Ile Glu
            125            130            135
Ser Ile Cys Asn Asp Pro Gly Ile Ile Ala Glu Asn Ile Arg Gln
            140            145            150
Val Lys Leu Gly Ser Pro Asp Tyr Ile Asp Cys Asp Arg Glu Lys
            155            160            165
Val Leu Glu Asp Phe Leu Lys Arg Ile Glu Cys Tyr Glu Val Asn
            170            175            180
Tyr Gln Pro Leu Asp Glu Glu Leu Asp Arg Ser Ser Thr Trp Ala
            185            190            195
His Ala Thr Trp

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<210> 6

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<212> PRT

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 7524680CD1

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Tyr Arg Arg Glu Ala Val Ser Tyr Lys Asn Tyr Glu Phe Phe Leu
            20             25             30

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His	Val	Ala	Val	Phe	Asp	Ala	Thr	Asn	Thr	Thr	Arg	Glu	Arg	Arg	65	70	75
Ser	Leu	Ile	Leu	Gln	Phe	Ala	Lys	Glu	His	Gly	Tyr	Lys	Val	Phe	80	85	90
Phe	Ile	Glu	Ser	Ile	Cys	Asn	Asp	Pro	Gly	Ile	Ile	Ala	Glu	Asn	95	100	105
Ile	Arg	Gln	Val	Lys	Leu	Gly	Ser	Pro	Asp	Tyr	Ile	Asp	Cys	Asp	110	115	120
Arg	Glu	Lys	Val	Leu	Glu	Asp	Phe	Leu	Lys	Arg	Ile	Glu	Cys	Tyr	125	130	135
Glu	Val	Asn	Tyr	Gln	Pro	Leu	Asp	Glu	Glu	Leu	Asp	Ser	His	Leu	140	145	150
Ser	Tyr	Ile	Lys	Ile	Phe	Asp	Val	Gly	Thr	Arg	Tyr	Met	Val	Asn	155	160	165
Arg	Val	Gln	Asp	His	Ile	Gln	Ser	Arg	Thr	Val	Tyr	Tyr	Leu	Met	170	175	180
Asn	Ile	His	Val	Thr	Pro	Arg	Ser	Ile	Tyr	Leu	Cys	Arg	His	Gly	185	190	195
Glu	Ser	Glu	Leu	Asn	Ile	Arg	Gly	Arg	Ile	Gly	Gly	Asp	Ser	Gly	200	205	210
Leu	Ser	Val	Arg	Gly	Lys	Gln	Tyr	Ala	Tyr	Ala	Leu	Ala	Asn	Phe	215	220	225
Ile	Gln	Ser	Gln	Gly	Ile	Ser	Ser	Leu	Lys	Val	Trp	Thr	Ser	His	230	235	240
Met	Lys	Arg	Thr	Ile	Gln	Thr	Ala	Glu	Ala	Leu	Gly	Val	Pro	Tyr	245	250	255
Glu	Gln	Trp	Lys	Ala	Leu	Asn	Glu	Ile	Asp	Ala	Gly	Val	Cys	Glu	260	265	270
Glu	Met	Thr	Tyr	Glu	Glu	Ile	Gln	Glu	His	Tyr	Pro	Glu	Glu	Phe	275	280	285
Ala	Leu	Arg	Asp	Gln	Asp	Lys	Tyr	Arg	Tyr	Arg	Tyr	Pro	Lys	Gly	290	295	300
Glu	Ser	Tyr	Glu	Asp	Leu	Val	Gln	Arg	Leu	Glu	Pro	Val	Ile	Met	305	310	315
Glu	Leu	Glu	Arg	Gln	Glu	Asn	Val	Leu	Val	Ile	Cys	His	Gln	Ala	320	325	330
Val	Met	Arg	Cys	Leu	Leu	Ala	Tyr	Phe	Leu	Asp	Lys	Ser	Ser	Asp	335	340	345
Glu	Leu	Pro	Tyr	Leu	Lys	Cys	Pro	Leu	His	Thr	Val	Leu	Lys	Leu	350	355	360
Thr	Pro	Val	Ala	Tyr	Gly	Cys	Lys	Val	Glu	Ser	Ile	Tyr	Leu	Asn	365	370	375
Val	Glu	Thr	Val	Asn	Thr	His	Arg	Glu	Lys	Pro	Glu	Asn	Val	Asp	380	385	390
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Tyr																	

<210> 7

<211> 426

<212> PRT

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 7524757CD1

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Thr	Asn	Ser	Pro	Thr	Met	Val	Ile	Met	Val	Gly	Leu	Pro	Ala	Arg
				20					25					30
Gly	Lys	Thr	Tyr	Ile	Ser	Thr	Lys	Leu	Thr	Arg	Tyr	Leu	Asn	Trp
				35					40					45
Ile	Gly	Thr	Pro	Thr	Lys	Asp	Asn	Met	Glu	Ala	Leu	Gln	Ile	Arg
				50					55					60
Lys	Gln	Cys	Ala	Leu	Ala	Ala	Leu	Lys	Asp	Val	His	Asn	Tyr	Leu
				65					70					75
Ser	His	Glu	Glu	Gly	His	Val	Ala	Val	Phe	Asp	Ala	Thr	Asn	Thr
				80					85					90
Thr	Arg	Glu	Arg	Arg	Ser	Leu	Ile	Leu	Gln	Phe	Ala	Lys	Glu	His
				95					100					105
Gly	Tyr	Lys	Val	Phe	Phe	Ile	Glu	Ser	Ile	Cys	Asn	Asp	Pro	Gly
				110					115					120
Ile	Ile	Ala	Glu	Asn	Ile	Arg	Gln	Val	Lys	Leu	Gly	Ser	Pro	Asp
				125					130					135
Tyr	Ile	Asp	Cys	Asp	Arg	Glu	Lys	Val	Leu	Glu	Asp	Phe	Leu	Lys
				140					145					150
Arg	Ile	Glu	Cys	Tyr	Glu	Val	Asn	Tyr	Gln	Pro	Leu	Asp	Glu	Glu
				155					160					165
Leu	Asp	Ser	His	Leu	Ser	Tyr	Ile	Lys	Ile	Phe	Asp	Val	Gly	Thr
				170					175					180
Arg	Tyr	Met	Val	Asn	Arg	Val	Gln	Asp	His	Ile	Gln	Ser	Arg	Thr
				185					190					195
Val	Tyr	Tyr	Leu	Met	Asn	Ile	His	Val	Thr	Pro	Arg	Ser	Ile	Tyr
				200					205					210
Leu	Cys	Arg	His	Gly	Glu	Ser	Glu	Leu	Asn	Ile	Arg	Gly	Arg	Ile
				215					220					225
Gly	Gly	Asp	Ser	Gly	Leu	Ser	Val	Arg	Gly	Lys	Gln	Tyr	Ala	Tyr
				230					235					240
Ala	Leu	Ala	Asn	Phe	Ile	Gln	Ser	Gln	Gly	Ile	Ser	Ser	Leu	Lys
				245					250					255
Val	Trp	Thr	Ser	His	Met	Lys	Arg	Thr	Ile	Gln	Thr	Ala	Glu	Ala
				260					265					270
Leu	Gly	Val	Pro	Tyr	Glu	Gln	Trp	Lys	Ala	Leu	Asn	Glu	Ile	Asp
				275					280					285
Ala	Gly	Val	Cys	Glu	Glu	Met	Thr	Tyr	Glu	Glu	Ile	Arg	Glu	His
				290					295					300
Tyr	Pro	Glu	Glu	Phe	Ala	Leu	Arg	Asp	Gln	Asp	Lys	Tyr	Arg	Tyr
				305					310					315
Arg	Tyr	Pro	Lys	Gly	Glu	Ser	Tyr	Glu	Asp	Leu	Val	Gln	Arg	Leu
				320					325					330
Glu	Pro	Val	Ile	Met	Glu	Leu	Glu							